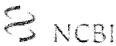
Exhibit B



Conserved Domain Database

1/2

`	UD I							
PubMed	Nucleotide	Protein	Str	ucture	CDO	Т	axonomy	Help?
CD: pfa	m02877.8, PARP_reg		PSSM-Id:	3371		Source	: Pfam[US],	Pfam[UK]
itsel com	r(ADP-ribose) polymerase, regul f and to a limited number of oth ponent induced by DNA damag loxyl 40 kDa fragment is still ca	er DNA binding pro ge. The carboxyl-te	oteins, which d	ecreases their	r affinity for DNA. Po	oly(ADP-ribos	se) polymerase	is a regulatory
Taxa: Eukaryota			References: 3 Pubmed Links					
Status: Alignment from source			Created: 11-Apr-2003					
Aligned: 6 rows			PSSM: 134 columns Representative: Consensus					
Proteins: [Clic	k here for CDART summary of	Proteins containing	g.pfam02877]					
Viou 31	Structure [Cn3D		'irtual Bor	vde 🚚			
A IEW O	y Su dicture with 10	מפווכ	using V	iiluai DOI	IUS (To displa	ay structure,	download Cn3[2)
View Ali	gnment as Hype	rtavt	- Widt	th 60 😾	color at 2.0 bits	- I		
VICW 7	as ji iype	i i C X i] widi	00	color at 2.0 Dit	است		
Subset F	Sewa 1 Luc to 10	- f + b			- 2.000			
Subsetr	Rows up to 10	of the mo	st aiverse	members				
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	10	20	30	40	50	60		
	*	*	*.		* *			
onsensus	1 FSKLLKSVQDLIKLI	FDVDSMAQTMME	FEIDMER	MPLGKLSFI	RQIQSAYRVLHEI	IYEV 58		
PAX	9 KSKLAFPIQDLIKMI	FDVESMKKAMVE	FEIDLOM	MPLGKLSKI	POIOSAYSILNE	700A 66		
1353140	171 LLHOLK-FNEAFGRP	IDCLSLACLTTG	YEILSKIEE	SIGGKSARI	RSTRGRPRVADRV	TLAV 229		
	295 OSKLDTRVAKEISLI	CHUSHMACHMME	TGYHAHE	TELGETSE.	STISKGYEVLKRI	SEV 343		
	**	FDIDSMNKTLME			ANTOGRVENUVERT	YNV 701		
1709741					NGT Sometical alm i			
1709741	•							
	70 *	80	90	100	110	120		
	· ·							
nsensus	59 ISDGGSPARLIDLSW	retimination.			ROMLDALK-EIEV			
AX	#7 VODGGSESQILDLSM				JOMLDNLL-DIEV			
	200 RSEGESLHDI-N	KYYSLIPHSFGF	CABBKID	SHAKIÇAE	RELLDALKgSIEA	ASLE 283		
1709740	344 I-DRYDRTRLEELSG	BFYTVI PHDFGF	KKMSqfVID	TPQKLKQKI	EHVEALG-EIEI	ATK 401		
548585	702 LEGGSHTAKLIDATN	PFYTLIPHNEGV	OLFTLIE	THOOISDLE	ROMLDSLA-ELEV	7AYS 758		
1709741	705 IQGGGTHAKFIDATN	RFYTLIPHNFGT	QSPPLLD	TTEQVEQL	QMLDSLI-EIEC	AYS 761		
	130							
	*							
nsensus	116 LLDLEDTASDKDPLD	PHYE 134						
	124 LLRGGNEDGDEDFID							
and the same of th	184 LEDLEKTASSEDIYO.							
	402 LLSVDPGLQD~DFLY							
	769 IIKSEDVSDACNPLD	~						
1709741	761 blotedskadinpid	nnib (5U						

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